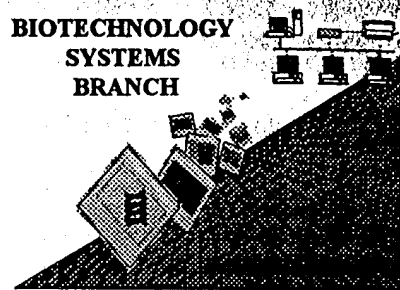


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/956,518

Art Unit / Team No. :

1645

Date Processed by STIC:

1/21/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

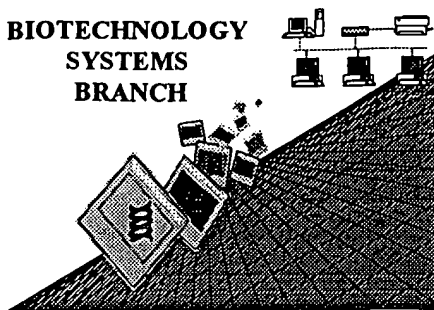
08/956,578

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
- 7 ☐ **Wrong Designation** Sequence(s) ____ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ **Use of N's or Xaa's (NEW RULES)** Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 ☐ **Wrong Format** File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.
AKS-Biotechnology Systems Branch- 7/10/98

BIOTECHNOLOGY
SYSTEMS
BRANCH



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: `pub/checker/`
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

*For Further Information, Contact: **Arti Shah at 703-308-4212***

R Hayes

1645

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518

DATE: 01/21/99
TIME: 15:21:10

INPUT SET: S30866.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Leonard, Sherry
Freedman, Robert

(ii) TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR

(iii) NUMBER OF SEQUENCES: 121

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MEDLEN & CARROLL, LLP
(B) STREET: 220 Montgomery Street, Suite 2200
(C) CITY: San Francisco
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/956,518
(B) FILING DATE: 23-OCT-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MacKnight, Kamrin T.
(B) REGISTRATION NUMBER: 38,230
(C) REFERENCE/DOCKET NUMBER: UTC-03042

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-705-8410
(B) TELEFAX: 415-397-8338

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:11

INPUT SET: S30866.raw

185 (2) INFORMATION FOR SEQ ID NO:9:
186
187 (i) SEQUENCE CHARACTERISTICS:
--> 188 (A) LENGTH: 337 base pairs
189 (B) TYPE: nucleic acid
190 (C) STRANDEDNESS: single
191 (D) TOPOLOGY: linear
192
193 (ii) MOLECULE TYPE: other nucleic acid
194 (A) DESCRIPTION: /desc = "DNA"
195
196
197
198
199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
200
201 AGATGCCCAA GTGGACCAGA GTCATCCTTC TGAAC'TGGTG CGCGTGGTTC
--> 202 CTGCGAATGA 60
203
204 AGAGGCCCGG GGAGGACAAG GTGCGCCCGG CCTGCCAGCA CAAGCAGCGG
--> 205 CGCTGCAGCC 120
206
207 TGGCCAGTGT GGAGATGAGC GCCGTGGGCC CGCCGCCCGC CAGCAACGGG
--> 208 AACCTGCTGT 180
209
210 ACATCGGCTT CCGCGGCCTG GACGGCGTGC ACTGTGTCCC GACCCCCGAC
--> 211 TCTGGGGTAG 240
212
213 TGTGTGGCCG CATGGCCTGC TCCCCACGC ACGATGAGCA CCTCCTGCAC
--> 214 GCGGGGCAAC 300
215
216 CCCCCGAGGG GGACCCGGAC TTGGCCAAGA TCCTGGA 337
217

(see item 1 on
Erra summary sheet)
format erra

236 (2) INFORMATION FOR SEQ ID NO:11:
237
238 (i) SEQUENCE CHARACTERISTICS:
--> 239 (A) LENGTH: 54 base pairs
240 (B) TYPE: nucleic acid
241 (C) STRANDEDNESS: single
242 (D) TOPOLOGY: linear
243
244 (ii) MOLECULE TYPE: other nucleic acid
245 (A) DESCRIPTION: /desc = "DNA"
246
247
248
249
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
251
252 CACACACACA TCACACACAC ACACACACAC ACACATACAC ACACACACCA CACA
253 54
254

same
erra

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:11

INPUT SET: S30866.raw

921 (2) INFORMATION FOR SEQ ID NO:49:
922
923 (i) SEQUENCE CHARACTERISTICS:
--> 924 (A) LENGTH: 48 base pairs
925 (B) TYPE: nucleic acid
926 (C) STRANDEDNESS: single
927 (D) TOPOLOGY: linear
928
929 (ii) MOLECULE TYPE: other nucleic acid
930 (A) DESCRIPTION: /desc = "DNA"
931
932
933
934
935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
936
937 CAUCAUCAUC AUCCAGCGTA CATCGATGTA GCAGGAAGTC TTGAATAT
938 48
939

940 (2) INFORMATION FOR SEQ ID NO:50:
941
942 (i) SEQUENCE CHARACTERISTICS:
--> 943 (A) LENGTH: 41 base pairs
944 (B) TYPE: nucleic acid
945 (C) STRANDEDNESS: single
946 (D) TOPOLOGY: linear
947
948 (ii) MOLECULE TYPE: other nucleic acid
949 (A) DESCRIPTION: /desc = "DNA"
950
951
952 (ix) FEATURE:
953 (A) NAME/KEY: -
954 (B) LOCATION: 32..33
955 (D) OTHER INFORMATION: /note= "The residue at this
956 position is Inosine."
957
958 (ix) FEATURE:
959 (A) NAME/KEY: -
960 (B) LOCATION: 36..37
961 (D) OTHER INFORMATION: /note= "The residue at this
962 position is Inosine."
963
964 (ix) FEATURE:
965 (A) NAME/KEY: -
966 (B) LOCATION: 41..42
967 (D) OTHER INFORMATION: /note= "The residue at this
968 position is Inosine."
969
970
971 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

same

"C" at location 32 can only represent itself,
"G" at location 33 only represents itself. nothing else.

If you want location 32 to be Inosine, use "N".
Same with location 33.

same error

There are only 41 nucleic acids in the sequence

Inosine can only be represented by "N".

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:12

INPUT SET: S30866.raw

972

973 CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGGGGGG G

974 41

975

41

1570 (2) INFORMATION FOR SEQ ID NO:84:
1571
1572 (i) SEQUENCE CHARACTERISTICS:
--> 1573 (A) LENGTH: 55 base pairs
1574 (B) TYPE: nucleic acid
1575 (C) STRANDEDNESS: single
1576 (D) TOPOLOGY: linear
1577
1578 (ii) MOLECULE TYPE: other nucleic acid
1579 (A) DESCRIPTION: /desc = "DNA"
1580
1581
1582
1583
1584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
1585
1586 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCT
--> 1587 GCACG 55
1588

Same
env

1751 (2) INFORMATION FOR SEQ ID NO:94:
1752
1753 (i) SEQUENCE CHARACTERISTICS:
--> 1754 (A) LENGTH: 457 base pairs
1755 (B) TYPE: nucleic acid
1756 (C) STRANDEDNESS: single
1757 (D) TOPOLOGY: linear
1758
1759 (ii) MOLECULE TYPE: other nucleic acid
1760 (A) DESCRIPTION: /desc = "DNA"
1761
1762
1763
1764
1765 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
1766
1767 AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
--> 1768 CAGAGGCGCG 60
1769
1770 AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
--> 1771 ACCCAGCGCC 120
1772
1773 GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
--> 1774 GAGACGCTGG 180
1775
1776 CCCGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
--> 1777 TCACGTGGAG 240
1778

Same

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:13

INPUT SET: S30866.raw

1779 AGGCGCGCGG GGGCGGGGCG GGGCGGGGCG CGCGCCCGGC TCCTTAAAGG
--> 1780 CGCGCGAGCC 300
1781
1782 GAGCGGCGAG GTGCCTCTGT GGCCGCAGGC GCAGGCCCGG GCGACAGCCG
--> 1783 AGACGTGGAG 360
1784
1785 CGCGCCGGCT CGCTGCAGCT CCGGGACTCA ACATGCGCTG CTCGCCGGGA
--> 1786 GGCGTCTGGC 420
1787
1788 TGGCGCTGGC CGCGTCGCTC CTGCACGGTA AAGCCAC
1789

457

same

1790 (2) INFORMATION FOR SEQ ID NO:95:
1791
1792 (i) SEQUENCE CHARACTERISTICS:
--> 1793 (A) LENGTH: 308 base pairs
1794 (B) TYPE: nucleic acid
1795 (C) STRANDEDNESS: single
1796 (D) TOPOLOGY: linear
1797
1798 (ii) MOLECULE TYPE: other nucleic acid
1799 (A) DESCRIPTION: /desc = "DNA"
1800
1801
1802
1803
1804 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
1805
1806 CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCCCT TGCCATTTTC
--> 1807 CAGCCGCGTC 60
1808
1809 CCACGAGGGT CACGGCGGCG GGGAGAGGTG GAGCCGCGAG AGCTCGGCCG
--> 1810 GGGGCCCCCGC 120
1811
1812 CTGGTGGCCG CGGCCATGAC AGCGGCTCGG GACTGGCTCC TTTTCCGCGC
--> 1813 CCTCCCGCC 180
1814
1815 GGAGGTGAGG GGAAGATGTC CATGTCAGGG TTCAAGGCCA AACCGAAGTT
--> 1816 ACTGGCCCTC 240
1817
1818 TATCTTCCAG GAGAACCAGG AGCCACAGCC GCGGCTCAG CCCCACCGCA
--> 1819 ACATTAAGGT 300
1820
1821 GAGTCGCC
1822

308

same

1823 (2) INFORMATION FOR SEQ ID NO:96:
1824
1825 (i) SEQUENCE CHARACTERISTICS:
--> 1826 (A) LENGTH: 145 base pairs
1827 (B) TYPE: nucleic acid
1828 (C) STRANDEDNESS: single
1829 (D) TOPOLOGY: linear

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:14

INPUT SET: S30866.raw

1830
1831 (ii) MOLECULE TYPE: other nucleic acid
1832 (A) DESCRIPTION: /desc = "DNA"
1833
1834
1835
1836
1837 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
1838
1839 CTCATTTCAG ATTACAAGTG GACACCTGAG TCAGCAGGAC CTGGAATCCC
--> 1840 AGATGAGAGA 60
1841
1842 GCTTATCTAC ACGACTCAGA TCTTGTGTC ACCCCCATTA TTGACAATCC
--> 1843 AAAGGTGCAG 120
1844
1845 AAAGCACTCT GACAAGTGAG TTGTA 145
1846

1847 (2) INFORMATION FOR SEQ ID NO:97:
1848
1849 (i) SEQUENCE CHARACTERISTICS:
--> 1850 (A) LENGTH: 84 base pairs
1851 (B) TYPE: nucleic acid
1852 (C) STRANDEDNESS: single
1853 (D) TOPOLOGY: linear
1854
1855 (ii) MOLECULE TYPE: other nucleic acid
1856 (A) DESCRIPTION: /desc = "DNA"
1857
1858
1859
1860
1861 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
1862
1863 TTAACCACAG ATAATGAAAC AACCACCATC GGTAAATTT GATGCAAAAA
--> 1864 TATTGCATCT 60
1865
1866 ACCAGCATTT TCAGGTAGGA TCAT 84
1867

1868 (2) INFORMATION FOR SEQ ID NO:98:
1869
1870 (i) SEQUENCE CHARACTERISTICS:
--> 1871 (A) LENGTH: 67 base pairs
1872 (B) TYPE: nucleic acid
1873 (C) STRANDEDNESS: single
1874 (D) TOPOLOGY: linear
1875
1876 (ii) MOLECULE TYPE: other nucleic acid
1877 (A) DESCRIPTION: /desc = "DNA"
1878
1879
1880

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:15

INPUT SET: S30866.raw

1881
1882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
1883
1884 TTTATTCTAG TTCCAATTGC TAATCCAGCA TTTGTGGATA GCTGCAAACCT
--> 1885 GCGATATGTA 60
1886
1887 AGTAACA
1888

67

1889 (2) INFORMATION FOR SEQ ID NO:99:
1890
1891 (i) SEQUENCE CHARACTERISTICS:
--> 1892 (A) LENGTH: 100 base pairs
1893 (B) TYPE: nucleic acid
1894 (C) STRANDEDNESS: single
1895 (D) TOPOLOGY: linear
1896
1897 (ii) MOLECULE TYPE: other nucleic acid
1898 (A) DESCRIPTION: /desc = "DNA"
1899
1900
1901
1902
1903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
1904
1905 CTGTTTCTAG TGCTGATGAG CGCTTTGACG CCACATTCCA CACTAACGTG
--> 1906 TTGGTGAATT 60
1907
1908 CTTCTGGGCA TTGCCAGTAC CTGCCTCCAG GTAAGCTGCA
1909

100

1928 (2) INFORMATION FOR SEQ ID NO:101:
1929
1930 (i) SEQUENCE CHARACTERISTICS:
--> 1931 (A) LENGTH: 392 base pairs
1932 (B) TYPE: nucleic acid
1933 (C) STRANDEDNESS: single
1934 (D) TOPOLOGY: linear
1935
1936 (ii) MOLECULE TYPE: other nucleic acid
1937 (A) DESCRIPTION: /desc = "DNA"
1938
1939
1940
1941
1942 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
1943
1944 AGAACGCAAG GGAGAGGTAG AGCCTGGCCT TGGGCAGCCC CTGGCCTGGC
--> 1945 CAGAGGCGCC 60
1946
1947 AGGCCGAGAG CCCGCTCGGT GGAGACTGGG GGTGGAGGTG CCCGGAGCGT
--> 1948 ACCCAGCGCC 120
1949

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:16

INPUT SET: S30866.raw

1950 GGGAGTACCT CCCGCTCACA CCTCGGGCTG CAGTTCCCTG GGTGGCCGCC
--> 1951 GAGACGCTGG 180
1952
1953 CCGGGGCTGG AGGGATGGCG GGGCGGGGAC GGGGGCGGGG GCGGGGCTCG
--> 1954 TCACGTGGAG 240
1955
1956 AGGCGCGCGG GGGCGGGCGG GGC GGCGGGGCG CGCGCCCGGC TCCTTAAAGG
--> 1957 CGCGCGAGCC 300
1958
1959 GAGCGGCGAG GTGCCTCTGT GGCCGCAGGC GCAGGCCCGG GCGACAGCCG
--> 1960 AGACGTGGAG 360
1961
1962 CGCGCCGGCT CGCTGCAGCT CCGGGACTCA AC
1963

392

1964 (2) INFORMATION FOR SEQ ID NO:102:
1965
1966 (i) SEQUENCE CHARACTERISTICS:
--> 1967 (A) LENGTH: 689 base pairs
1968 (B) TYPE: nucleic acid
1969 (C) STRANDEDNESS: single
1970 (D) TOPOLOGY: linear
1971
1972 (ii) MOLECULE TYPE: other nucleic acid
1973 (A) DESCRIPTION: /desc = "DNA"
1974
1975
1976
1977
1978 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
1979
1980 AGCCCTTTCC CAGGCGGTAG CGGGGGCAGT GGTGCTGTTG CCCTTTTAAA
--> 1981 CTGCGGCTTG 60
1982
1983 ACGGGAGCCG CGCCTCCTGT CGGTGGAGTC GGTATAAAAG GGAGCAGCCC
--> 1984 CGCAGGCCGC 120
1985
1986 CACATAGCTC CCGCCAAGTC CTCGGTGCCC CTTGCCATTT TCCAGCCGCG
--> 1987 CTCCCACGAG 180
1988
1989 GGTCACGGCG GCGGGGAGAG GTGGAGCCGC GAGAGCTCGG CCGGGGGCCC
--> 1990 CGCCTGGTGG 240
1991
1992 CCGCGGCCAT GACAGCGGCT CGGGACTGGC TCCTTTTCCG CGCCCCTCCC
--> 1993 GCCGGAGGTG 300
1994
1995 AGGGGAAGAT GTCCATGTCA GGGTTCAAGG CCAAACCGAA GTTACTGGCC
--> 1996 TCTATCTTCC 360
1997
1998 AGGAGAACCA GGAGCCACAG CCGCGGCTCA CGCCCCACCG CAACATTAAG
--> 1999 ATTACAAGTG 420
2000
2001 GACACCTGAG TCAGCAGGAC CTGGAATCCC AGATGAGAGA GCTTATCTAC

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:16

INPUT SET: S30866.raw

--> 2002 ACGACTCAGA 480
2003
2004 TCTTGTTGTC ACCCCCATTA TTGACAATCC AAAGGTGCAG AAAGCACTCT
--> 2005 GACAATTCCA 540
2006
2007 ATTGCTAATC CAGCATTGTG GGATAGCTGC AAAGTGCAT ATTGCTGATG
--> 2008 AGCGCTTTGA 600
2009
2010 CGCCACATTC CACACTAACG TGTGGTGAA TTCTTCTGGG CATTGCCAGT
--> 2011 ACCTGCCTCC 660
2012
2013 AGGCATATTC AAGAGTTCCT GCTACATCG 689
2014

2015 (2) INFORMATION FOR SEQ ID NO:103:
2016
2017 (i) SEQUENCE CHARACTERISTICS:
--> 2018 (A) LENGTH: 641 base pairs
2019 (B) TYPE: nucleic acid
2020 (C) STRANDEDNESS: single
2021 (D) TOPOLOGY: linear
2022
2023 (ii) MOLECULE TYPE: other nucleic acid
2024 (A) DESCRIPTION: /desc = "DNA"
2025
2026
2027
2028
2029 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
2030
2031 CAGGCCGCCA CATAGCTCCC GCCAAGTCCT CGGTGCCCCCT TGCCATTTTC
--> 2032 CAGCCGCGCT 60
2033
2034 CCCACGAGGG TCACGGCGGC GGGGAGAGGT GGAGCCGCGA GAGCTCGGCC
--> 2035 GGGGGCCCCG 120
2036
2037 CCTGGTGGCC GCGGCCATGA CAGCGGCTCG GGACTGGCTC CTTTTCCGCG
--> 2038 CCCC'TCCCGC 180
2039
2040 CGGAGGTGAG GGAAGATGT CCATGTCAGG GTTCAAGGCC AAACCGAAGT
--> 2041 TACTGGCCTC 240
2042
2043 TATCTTCCAG GAGAACCAGG AGCCACAGCC GCGGCTCAGC CCCCACCGCA
--> 2044 ACATTAAGAT 300
2045
2046 TACAAGTGGA CACCTGAGTC AGCAGGACCT GGAATCCCAG ATGAGAGAGC
--> 2047 TTATCTACAC 360
2048
2049 GACTCAGATC TTGTTGTCAC CCCCAT'TATT GACAATCCAA AGGTGCAGAA
--> 2050 AGCACTCTGA 420
2051
2052 CAAATAATGA AACAAACCACC ATCGGT'TAAA TTTGATGCAA AAATATTGCA
--> 2053 TCTACCAGCA 480

same

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/956,518DATE: 01/21/99
TIME: 15:21:17

INPUT SET: S30866.raw

2054
2055 TTTTCAGTTC CAATTGCTAA TCCAGCATTT GTGGATAGCT GCAAACCTGCG
--> 2056 ATATTGCTGA 540
2057
2058 TGAGCGCTTT GACGCCACAT TCCACACTAA CGTGTGGTG AATTCTTCTG
--> 2059 GGCATTGCCA 600
2060
2061 GTACCTGCCT CCAGGCATAT TCAAGAGTTC CTGCTACATC G 641
2062

2081 (2) INFORMATION FOR SEQ ID NO:105:
2082
2083 (i) SEQUENCE CHARACTERISTICS:
--> 2084 (A) LENGTH: 140 base pairs
2085 (B) TYPE: nucleic acid
2086 (C) STRANDEDNESS: single
2087 (D) TOPOLOGY: linear
2088
2089 (ii) MOLECULE TYPE: other nucleic acid
2090 (A) DESCRIPTION: /desc = "DNA"
2091
2092
2093
2094
2095 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
2096
2097 TGTCCNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2098 NNNNNNNNNN 60
2099
2100 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2101 NNNNNNNNNN 120
2102
2103 NNNNNNNNNN NNNNGACGTG 140
2104

Same

2123 (2) INFORMATION FOR SEQ ID NO:107:
2124
2125 (i) SEQUENCE CHARACTERISTICS:
--> 2126 (A) LENGTH: 44 base pairs
2127 (B) TYPE: nucleic acid
2128 (C) STRANDEDNESS: single
2129 (D) TOPOLOGY: linear
2130
2131 (ii) MOLECULE TYPE: other nucleic acid
2132 (A) DESCRIPTION: /desc = "DNA"
2133
2134
2135
2136
2137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
2138
2139 GATGAGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCA AATG
2140 44

Same

INPUT SET: S30866.raw

2141

2160 (2) INFORMATION FOR SEQ ID NO:109:
2161
2162 (i) SEQUENCE CHARACTERISTICS:
--> 2163 (A) LENGTH: 110 base pairs
2164 (B) TYPE: nucleic acid
2165 (C) STRANDEDNESS: single
2166 (D) TOPOLOGY: linear
2167
2168 (ii) MOLECULE TYPE: other nucleic acid
2169 (A) DESCRIPTION: /desc = "DNA"
2170
2171
2172
2173
2174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
2175
2176 TCTTGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2177 NNNNNNNNNN 60
2178
2179 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNAACAG
2180 110
2181

2200 (2) INFORMATION FOR SEQ ID NO:111:
2201
2202 (i) SEQUENCE CHARACTERISTICS:
--> 2203 (A) LENGTH: 80 base pairs
2204 (B) TYPE: nucleic acid
2205 (C) STRANDEDNESS: single
2206 (D) TOPOLOGY: linear
2207
2208 (ii) MOLECULE TYPE: other nucleic acid
2209 (A) DESCRIPTION: /desc = "DNA"
2210
2211
2212
2213
2214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
2215
2216 GCTGATNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2217 NNNNNNNNNN 60
2218
2219 NNNNNNNNNN NNNCCTCCAG
2220

2239 (2) INFORMATION FOR SEQ ID NO:113:
2240
2241 (i) SEQUENCE CHARACTERISTICS:
--> 2242 (A) LENGTH: 168 base pairs
2243 (B) TYPE: nucleic acid
2244 (C) STRANDEDNESS: single

80

RAW SEQUENCE LISTING
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2245 (D) TOPOLOGY: linear
2246
2247 (ii) MOLECULE TYPE: other nucleic acid
2248 (A) DESCRIPTION: /desc = "DNA"
2249
2250
2251
2252
2253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
2254
2255 GCATANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2256 NNNNNNNNNN 60
2257
2258 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2259 NNNNNNNNNN 120
2260
2261 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NCTAGTGG
2262 168
2263

2282 (2) INFORMATION FOR SEQ ID NO:115:
2283
2284 (i) SEQUENCE CHARACTERISTICS:
--> 2285 (A) LENGTH: 195 base pairs
2286 (B) TYPE: nucleic acid
2287 (C) STRANDEDNESS: single
2288 (D) TOPOLOGY: linear
2289
2290 (ii) MOLECULE TYPE: other nucleic acid
2291 (A) DESCRIPTION: /desc = "DNA"
2292
2293
2294
2295
2296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
2297
2298 GAATCNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2299 NNNNNNNNNN 60
2300
2301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2302 NNNNNNNNNN 120
2303
2304 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2305 NNNNNNNNNN 180
2306
2307 NNNNNNNNTC CCTGG
2308

2327 (2) INFORMATION FOR SEQ ID NO:117:
2328
2329 (i) SEQUENCE CHARACTERISTICS:
--> 2330 (A) LENGTH: 87 base pairs
2331 (B) TYPE: nucleic acid

195

RAW SEQUENCE LISTING
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INPUT SET: S30866.raw

2332 (C) STRANDEDNESS: single
2333 (D) TOPOLOGY: linear
2334
2335 (ii) MOLECULE TYPE: other nucleic acid
2336 (A) DESCRIPTION: /desc = "DNA"
2337
2338
2339
2340
2341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
2342
2343 GGATANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2344 NNNNNNNNNN 60
2345
2346 NNNNNNNNNN NNNNNNNNNN TTGATAG 87
2347

2366 (2) INFORMATION FOR SEQ ID NO:119:
2367
2368 (i) SEQUENCE CHARACTERISTICS:
--> 2369 (A) LENGTH: 110 base pairs
2370 (B) TYPE: nucleic acid
2371 (C) STRANDEDNESS: single
2372 (D) TOPOLOGY: linear
2373
2374 (ii) MOLECULE TYPE: other nucleic acid
2375 (A) DESCRIPTION: /desc = "DNA"
2376
2377
2378
2379
2380 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
2381
2382 CCCAGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2383 NNNNNNNNNN 60
2384
2385 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNAAGTGG
2386 110
2387

2406 (2) INFORMATION FOR SEQ ID NO:121:
2407
2408 (i) SEQUENCE CHARACTERISTICS:
--> 2409 (A) LENGTH: 519 base pairs
2410 (B) TYPE: nucleic acid
2411 (C) STRANDEDNESS: single
2412 (D) TOPOLOGY: linear
2413
2414 (ii) MOLECULE TYPE: other nucleic acid
2415 (A) DESCRIPTION: /desc = "DNA"
2416
2417
2418

RAW SEQUENCE LISTING
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INPUT SET: S30866.raw

2419
2420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
2421
2422 ACCAGANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2423 NNNNNNNNNN 60
2424
2425 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2426 NNNNNNNNNN 120
2427
2428 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2429 NNNNNNNNNN 180
2430
2431 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2432 NNNNNNNNNN 240
2433
2434 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2435 NNNNNNNNNN 300
2436
2437 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2438 NNNNNNNNNN 360
2439
2440 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2441 NNNNNNNNNN 420
2442
2443 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
--> 2444 NNNNNNNNNN 480
2445
2446 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
2447 519
2448

same

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/956,518

DATE: 01/21/99

TIME: 15:21:23

INPUT SET: S30866.raw

Line	Error	Original Text
188	Entered (337) and Calc. Seq. Length (87) differ	(A) LENGTH: 337 base pairs
202	# of Sequences for line conflicts w/ running total	CTGCGAATGA 60
205	# of Sequences for line conflicts w/ running total	CGCTGCAGCC 120
208	# of Sequences for line conflicts w/ running total	AACCTGCTGT 180
211	# of Sequences for line conflicts w/ running total	TCTGGGGTAG 240
214	# of Sequences for line conflicts w/ running total	GGCGGGCAAC 300
239	Entered (54) and Calc. Seq. Length (0) differ	(A) LENGTH: 54 base pairs
924	Entered (48) and Calc. Seq. Length (0) differ	(A) LENGTH: 48 base pairs
943	Entered (41) and Calc. Seq. Length (0) differ	(A) LENGTH: 41 base pairs
1573	Entered (55) and Calc. Seq. Length (5) differ	(A) LENGTH: 55 base pairs
1587	# of Sequences for line conflicts w/ running total	GCACG 55
1754	Entered (457) and Calc. Seq. Length (107) differ	(A) LENGTH: 457 base pairs
1768	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1771	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1774	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1777	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1780	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1783	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1786	# of Sequences for line conflicts w/ running total	GGCGTCTGGC 420
1793	Entered (308) and Calc. Seq. Length (58) differ	(A) LENGTH: 308 base pairs
1807	# of Sequences for line conflicts w/ running total	CAGCCGCGTC 60
1810	# of Sequences for line conflicts w/ running total	GGGGCCCCGC 120
1813	# of Sequences for line conflicts w/ running total	CCCTCCCCGC 180
1816	# of Sequences for line conflicts w/ running total	ACTGGCCCTC 240
1819	# of Sequences for line conflicts w/ running total	ACATTAAGGT 300
1826	Entered (145) and Calc. Seq. Length (45) differ	(A) LENGTH: 145 base pairs
1840	# of Sequences for line conflicts w/ running total	AGATGAGAGA 60
1843	# of Sequences for line conflicts w/ running total	AAAGGTGCAG 120
1850	Entered (84) and Calc. Seq. Length (34) differ	(A) LENGTH: 84 base pairs
1864	# of Sequences for line conflicts w/ running total	TATTGCATCT 60
1871	Entered (67) and Calc. Seq. Length (17) differ	(A) LENGTH: 67 base pairs
1885	# of Sequences for line conflicts w/ running total	GCGATATGTA 60
1892	Entered (100) and Calc. Seq. Length (50) differ	(A) LENGTH: 100 base pairs
1906	# of Sequences for line conflicts w/ running total	TTGGTGAATT 60
1931	Entered (392) and Calc. Seq. Length (92) differ	(A) LENGTH: 392 base pairs
1945	# of Sequences for line conflicts w/ running total	CAGAGGCGCG 60
1948	# of Sequences for line conflicts w/ running total	ACCCAGCGCC 120
1951	# of Sequences for line conflicts w/ running total	GAGACGCTGG 180
1954	# of Sequences for line conflicts w/ running total	TCACGTGGAG 240
1957	# of Sequences for line conflicts w/ running total	CGCGCGAGCC 300
1960	# of Sequences for line conflicts w/ running total	AGACGTGGAG 360
1967	Entered (689) and Calc. Seq. Length (139) differ	(A) LENGTH: 689 base pairs
1981	# of Sequences for line conflicts w/ running total	CTGCGGCTTG 60
1984	# of Sequences for line conflicts w/ running total	CGCAGGCCGC 120
1987	# of Sequences for line conflicts w/ running total	CTCCACGAG 180
1990	# of Sequences for line conflicts w/ running total	CGCCTGGTGG 240
1993	# of Sequences for line conflicts w/ running total	GCCGGAGGTG 300
1996	# of Sequences for line conflicts w/ running total	TCTATCTTCC 360

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/956,518

DATE: 01/21/99
TIME: 15:21:24

INPUT SET: S30866.raw

Line	Error	Original Text
1999	# of Sequences for line conflicts w/ running total	ATTACAAGTG 420
2002	# of Sequences for line conflicts w/ running total	ACGACTCAGA 480
2005	# of Sequences for line conflicts w/ running total	GACAATTCCA 540
2008	# of Sequences for line conflicts w/ running total	AGCGCTTTGA 600
2011	# of Sequences for line conflicts w/ running total	ACCTGCCTCC 660
2018	Entered (641) and Calc. Seq. Length (141) differ	(A) LENGTH: 641 base pairs
2032	# of Sequences for line conflicts w/ running total	CAGCCGCGCT 60
2035	# of Sequences for line conflicts w/ running total	GGGGGCCCCG 120
2038	# of Sequences for line conflicts w/ running total	CCCCTCCCGC 180
2041	# of Sequences for line conflicts w/ running total	TACTGGCCTC 240
2044	# of Sequences for line conflicts w/ running total	ACATTAAAGAT 300
2047	# of Sequences for line conflicts w/ running total	TTATCTACAC 360
2050	# of Sequences for line conflicts w/ running total	AGCACTCTGA 420
2053	# of Sequences for line conflicts w/ running total	TCTACCAGCA 480
2056	# of Sequences for line conflicts w/ running total	ATATTGCTGA 540
2059	# of Sequences for line conflicts w/ running total	GGCATTGCCA 600
2084	Entered (140) and Calc. Seq. Length (40) differ	(A) LENGTH: 140 base pairs
2098	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2101	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2126	Entered (44) and Calc. Seq. Length (0) differ	(A) LENGTH: 44 base pairs
2163	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs
2177	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2203	Entered (80) and Calc. Seq. Length (30) differ	(A) LENGTH: 80 base pairs
2217	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2242	Entered (168) and Calc. Seq. Length (20) differ	(A) LENGTH: 168 base pairs
2256	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2259	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2285	Entered (195) and Calc. Seq. Length (45) differ	(A) LENGTH: 195 base pairs
2299	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2302	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2305	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 180
2330	Entered (87) and Calc. Seq. Length (37) differ	(A) LENGTH: 87 base pairs
2344	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2369	Entered (110) and Calc. Seq. Length (10) differ	(A) LENGTH: 110 base pairs
2383	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2409	Entered (519) and Calc. Seq. Length (80) differ	(A) LENGTH: 519 base pairs
2423	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 60
2426	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 120
2429	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 180
2432	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 240
2435	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 300
2438	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 360
2441	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 420
2444	# of Sequences for line conflicts w/ running total	NNNNNNNNNN 480